

FIG. 1A

Input file Fb18903FL.seq; Output File 18903.trans
Sequence length 1983

```

CCTTTAGCCAATTGCGCGAGGCTCCGCCCCAGTACTTGTCGGCAGGATTAAAGCAGATAAAGTGTGCTCACAC
      M P S T V L P S T V L P S L L 15
ACTGTAGACACGGCTACC ATG CCA TCC ACA GTG TTG CCA TCC ACA GTG TTG CCA TCA CTC CTG 45

P T A G A G W S M R W I L C W S L T L C 35
CCC ACA GCA GGA GCT GGC TGG AGC ATG AGG TGG ATT CTG TGC TGG AGC CTC ACC CTC TGC 105

L M A Q T A L G A L H T K R P Q V V T K 55
CTG ATG GCG CAG ACG GCC TTG GGT GCC TTG CAC ACC AAG AGG CCT CAA GTG GTC ACC AAA 165

Y G T L Q G K Q M H V G K T P I Q V F L 75
TAT GGA ACC CTG CAA GGA AAA CAG ATG CAT GTG GGG AAG ACA CCC ATC CAA GTG TTT TTA 225

G V P F S R P P L G I L R F A P P E P P 95
GGA GTC CCC TTC TCC AGA CCT CCT CTA GGT ATC CTC AGG TTT GCA CCT CCA GAA CCC CCG 285

E P W K G I R D A T T Y P P G C L Q E S 115
GAG CCC TGG AAA GGA ATC AGA GAT GCT ACC ACC TAC CCG CCT GGG TGC CTG CAG GAG TCC 345

W G Q L A S M Y V S T R E R Y K W L R F 135
TGG GGC CAG CTG GCC TCG ATG TAC GTC AGC ACG CGG GAA CGG TAC AAG TGG CTG CGC TTC 405

S E D C L Y L N V Y A P A R A P G D P Q 155
AGC GAG GAC TGT CTG TAC CTG AAC GTG TAC GCG CCG GCG GCG GCG CCC GGG GAT CCC CAG 465

L P V M V W F P G G A F I V G A A S S Y 175
CTG CCA GTG ATG GTC TGG TTC CCG GGA GGC GCC TTC ATC GTG GGC GCT GCT TCT TCG TAC 525

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FIG. 1B

E G S D L A A R E K V V L V F L Q H R L 195
 GAG GGC TCT GAC TTG GCC CGC GAG AAA GTG GTG CTG TTT CTG CAG CAC AGG CTC 585

 G I F G F L S T D S H A R G N W G L L 215
 GGC ATC TTC GGC TTC AGC ACG GAC GAC CGC CGC GGG AAC TGG GGG CTG CTG 645

 D Q M A A L R W V Q E N I A A F G G D P 235
 GAC CAG ATG GCG GCT CTG CGC TGG GTG CAG GAG AAC ATC GCA GCC TTC GGG GGA GAC CCA 705

 G N V T L F G Q S A G A M S I S G L M M 255
 GGA AAT GTG ACC CTG TTC GGC CAG TCG GCG GCG GCC ATG AGC ATC TCA GGA CTG ATG ATG 765

 S P L A S G L F H R A I S Q S G T A L F 275
 TCA CCC CTA GCC TCG GGT CTC TTC CAT CGG GCC ATT TCC CAG AGT GGC ACC GCG TTA TTC 825

 R L F I T S N P L K V A K K V A H L A G 295
 AGA CTT TTC ATC ACT AGT AAC CCA CTG AAA GTG GCC AAG AAG GTT GCC CAC CTG GCT GGA 885

 C N H N S T Q I L V N C L R A L S G T K 315
 TGC AAC CAC AAC AGC ACA CAG ATC CTG GTA AAC TGC CTG AGG GCA CTA TCA GGG ACC AAG 945

 V M R V S N K M R F L Q L N F Q R D P E 335
 GTG ATG CGT GTG TCC AAC AAG ATG AGA TTC CTC CAA CTG AAC TTC CAG AGA GAC CCG GAA 1005

 E I I W S M S P V V D G V V I P D D P L 355
 GAG ATT ATC TGG TCC ATG AGC CCT GTG GTG GAT GGT GTG CTG ATC CCA GAT GAC CCT TTG 1065

 V L L T Q G K V S S V P Y L L G V N N L 375
 GTG CTC CTG ACC CAG GGG AAG GTT TCA TCT GTG CCC TAC CTT CTA GGT GTC AAC AAC CTG 1125

 E F N W L L P Y I M K F P L N R Q A M R 395
 GAA TTC AAT TGG CTC TTG CCT TAT ATC ATG AAG TTC CCG CTA AAC CCG CAG GCG ATG AGA 1185

FIG. 1C

K E T I T K M L W S T R T L L N I T K E 415
 AAG GAA ACC ATC ACT AAG ATG CTC TGG AGT ACC CGC ACC CTG TTG AAT ATC ACC AAG GAG 1245
 Q V P L V V E E Y L D N V N E H D W K M 435
 CAG GTA CCA CTT GTG GTG GAG GAG TAC CTG GAC AAT GTC AAT GAG CAT GAC TGG AAG ATG 1305
 L R N R M M D I V Q D A T F V Y A T L Q 455
 CTA CGA AAC CGT ATG ATG GAC ATA GTT CAA GAT GCC ACT TTC GTG TAT GCC ACA CTG CAG 1365
 T A H Y H R D A G L P V Y L Y E F E H H 475
 ACT GCT CAC TAC CAC GAT GCC GGC CTC CCT GTC TAC CTG TAT GAA TTT GAG CAC CAC 1425
 A R G I I V K P R T D G A D H G D E M Y 495
 GCT CGT GGA ATA ATC GTC AAA CCC CGC ACT GAT GGG GCA GAC CAT GGG GAT GAG ATG TAC 1485
 F L F G G P F A T G L S M G K E K A L S 515
 TTC CTC TTT GGG GGC CCC TTC GCC ACA GGC CTT TCC ATG GGT AAG GAG AAG GCA CTT AGC 1545
 L Q M M K Y W A N F A R T G N P N D G N 535
 CTC CAG ATG ATG AAA TAC TGG GCC AAC TTT GCC CGC ACA GGA AAC CCC AAT GAT GGG AAT 1605
 L P C W P R Y N K D E K Y L Q L D F T T 555
 CTG CCC TGC TGG CCA CGC TAC AAC AAG GAT GAA AAG TAC CTG CAG CTG GAT TTT ACC ACA 1665
 R V G M K L K E K K M A F W M S L Y Q S 575
 AGA GTG GGC ATG AAG CTC AAG GAG AAG AAG ATG GCT TTT TGG ATG AGT CTG TAC CAG TCT 1725
 Q R P E K Q R Q F *
 CAA AGA CCT GAG AAG CAG AGG CAA TTC TAA 585
 1755

GGGTGGCTATGCAGGAAGGCCAAAGAGGGGTTTGCCCCACCATCCAGGCCTGGGGAGATGACCATGGACATAC

TGGGACAAAGATTCTACCCAAAGGCCGAATTCGTTTAAACCTGCAGGATAG

FIG. 2

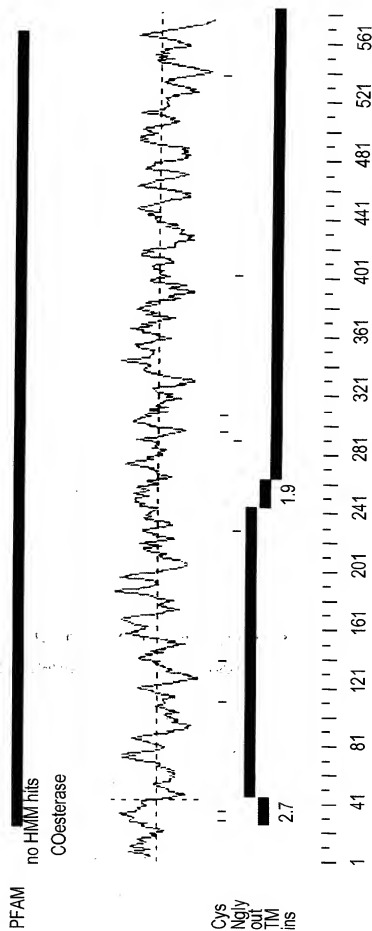


FIG. 3A

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM

hmmfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

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HMMER is freely distributed under the GNU General Public License (GPL).

HMM file:

/prod/ddm/seqanal/PFAM/pfam6.4/Pfam

Sequence file:

/prod/ddm/wspace/orfanal/oa-script.6214.seq

Query: Fbh18903FL

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
COesterase	Carboxylesterase	558.6	4.1e-164	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
COesterase	1/1	25	569	1	612	558.6	4.1e-164

Alignments of top-scoring domains:

COesterase: domain 1 of 1, from 25 to 569: score 558.6, E = 4.1e-164

*-2mvlilllflillllliavlaaakaspdpillvatnnVlcgkvrGvnek

+1+ +L 1 1 ++ +1+a+++ ++ V t++ G++ G++

18903 25 RWILCWSLITCLMAQTALGALT---KRPQVTKY----GTLQKQKH 65

tdngeqvysfLGIPIYAepPVGnlRfKaPqPyKepWsdvldAtkyppsCI

+ ++ +FLG+P+ PP+G IRF +P+ +epW++++dat+YpP CI

18903 66 VGKT--PIQVFLGVFFSRPELILRFAPPEP-PEPWKINDATTYPGCL 112

FIG. 3B

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QdddfgsldkValkmlslgnklvg....lklsEDCLYLNvYtPknt
Q + +g+ 1 +++ ++ + + 1 +sEDCLYLNvY P+ +
18903 113 Q-ESWQ-----LASMVSTREYkwlRFSEDCLYLNvYAPARA 150

kpnkklPmVwVlhGGGfmgshslpslydgeslaregnVivVsINYRL
+ + +lFVmVw +GG+F +G++ s+Y g+ la+++V++V ++ RL
18903 151 PGDPQLPVMWfPGGAfIVGAA-----SSYEGSDLAAREKVLVFLQHRL 195

GpLGFLstgdklpGsgNYCLLDQrIALkVWqDNiaafGCDPnsVtIfge
G++GFLst+d+++ GN+GLLDQ +AL+VWq+NiaafGCDP++VT+fG+
18903 196 GfGFLSTDDSHAR--GNWGLDQMAALRWQENIAAFGCDPGCVTLFGQ 243

SAGaaSVsllllngDnpsskGLFhRAIsqSGsalspwaigsesnarg
SAGa+S+s l++s p++ GLFhRAIsqSG+al ++s+ +
18903 244 SAGAMsISGLMS-----PLA-SGLFhRAIsqSGTALFRlFITSNP--LK 285

rakelarllGcnetssellDCLRsksaeLleatrsfllfeyvpflpf
ak++a l+Gcn++s l+ CLR s + + + + + f + +f +
18903 286 VAKKVAHLACGNHNSTQILVNCILRALSGTKVMRVSNK-NRFLQLNFQDP 334

l....aFgPvDGDapeafipeelikeGkfadvPyliGvtdEGy
++ + +PvDg+ +ip+dP+ l+ +Gk + vPyl Gv++ E+ +
18903 335 EeiwSNsPVDGV-----VIPDDPLVLTQGVSSVPYllGVNLFNW 379

faamllnasggedelkketnpdvwlellkyllyasealnikdMddlad
+++ +++ + + ket ++ l+ ll+ + +
18903 380 LLPYMKFPLNR-QAMRKETITK-MLWSTRTILN-ITKEQ-----VP 418

kvlekyPgvdvdfsvesrkpnlqdmldllfkcptrvaadlhathggsPv
v e+Y++ v + + + + d++ D +F+++ + ++ +++g Pv
18903 419 LVVEEYLDVNEHDWKLRLNRMDIVQDATFYIA-TLQTAHYHRDAGLPV 467

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FIG. 3C

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YayvdpasfgigQflakrvdpfsggavhgdeiffvFgnpllkedlyka
Y+Y+f h+a+ + v+p+++ga+HgdE++f+fg p+ ++ l
18903 468 YLYEFHHAR-----GIIVKPRTDGADHGDEMYFLFGGPFATG-LS-- 507

teeeekssktmmywanFaktGnPnngtsnglvvWpkytseeqkyslli
e++ts +mm+yywanFA+tGnP n++ +l+ Wp y+++e +l+
18903 508 MGKEKALS-LQMKIYANFARTGNP-NDG--NLPCWPRYNKDEK--YIQL 551

llttitaqklkardprkvlcnfw<-*
+tt +klk+++ ++fw
18903 552 DFTTRVGMLKEKK-----MAFW 569

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Searching for complete domains in SMART

FIG. 4A

GAP of: FrGcgManager 76 IOA81nWg check: 5132 from: 1 to: 1983

Fbh18903FL - Import - vector trimmed

to: FrGcqManager 76 JOA3WXZ1 check: 1319 from: 1 to: 2456

z34105 in Patent Nucleotide

Symbol comparison table: /ddm local/qc9/qc9 9.1/

1/gcgcore/data/rundata/nwsgapdna.cmp

CompCheck: 8760

```

Gap Weight:      12      Average Match: 10.000
Length Weight:   4       Average Mismatch: 0.000

```

Quality:	13796	Length:	2746
Ratio:	6.957	Gaps:	14
Percent Similarity:	92.617	Percent Identity:	92.617

Match display thresholds for the alignment(s):

$$1 = \text{IDENTITY}$$
 $\vdots = 5$ $\gamma = 1$

```
FrGcqManager 76 IOA81nWq  x FrGcqManager 76 JOA3WXZ1
```

```

COE-2      1 .....CCT 3
Z34105 101 CATTTCGCCTTGCTGACGGCGTGAGCCCTGGCCAGACATGTCACAGGG 150
          4 TTAGCCAATTTCGGCCGAGGCGCTCCGCGCCCACTGTTGCTGGCAGGGAT 52
          | | | | | | | | | | | | | | | | | | | | | | | | | |
151 TTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACCGTGCCGCGCGGCGG 200
          | | | | | | | | | | | | | | | | | | | | | | | | | |
          53 TAAGAGCAGA.TAAAAAGTGTGCTCACACACTGTAGACACGGGTACCATGC 101
          | | | | | | | | | | | | | | | | | | | | | | | | | |
201 GACCAGCACAGGCGCGCTTTTCTCCTTCGGAACGGGAACGTCTAGCAACC 250
          | | | | | | | | | | | | | | | | | | | | | | | | | |
          102 CATC.....CACAGTGTGGCCATCCACAGTGTGGCCATCACTCTCTGC. 143
          | | | | | | | | | | | | | | | | | | | | | | | | | |
251 CTTCTGTGGGGCTCAATTTTGAAATCTTGAAAGTACTTCAACTCCAGCA 300
          | | | | | | | | | | | | | | | | | | | | | | | | | |
          144 .CCACAGCAGGAGCT..GGCTGGAGCATGAGTGGATTCTGTG..CTGGA 188
          | | | | | | | | | | | | | | | | | | | | | | | | | |
301 ACTACATCTGCTCCCTCAAGTGGTTTGGAAACCGGGCTCTTTGGATCTAA 350
          | | | | | | | | | | | | | | | | | | | | | | | | | |

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189 GCCTCACACCT...CTGCCTGATGGCGCAGACGCCCTTGGGTGCCTTGCACT 235
||| || | | | | | | |
351 ACCTGCCACTGGGTTCACTCTAGGAGGA.ACAAATACAGGTGCCTTGCACT 399

236 ACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCTGCAAGGAAAAACA 285
|||||
400 ACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCTGCAAGGAAAAACA 449

286 GATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCTTCT 335
|||||
450 GATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCTTCT 499

336 CCAGACCTCCTCTAGGTATCCTCAGGTTTGACACCTCCAGAACCCCCGGAG 385
|||||
500 CCAGACCTCCTCTAGGTATCCTCAGGTTTGACACCTCCAGAACCCCCGGAG 549

386 CCCTGGAAGGAATCAGAGATGCTACCACCTACCCGCCTG..... 425
|||||
550 CCCTGGAAGGAATCAGAGATGCTACCACCTACCCGCCTGGATGGAGTCT 599

.
426GGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCGATGTA 465
|||||
700 TGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCGATGTA 749

466 CGTCAGCACGCGGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTC 515
|||||
750 CGTCAGCACGCGGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTC 799

516 TGTAACCTGAACGTGTACGCGCCGCGCGCGCCCGGGGATCCCCAGCTG 565
|||||
800 TGTAACCTGAACGTGTACGCGCCGCGCGCGCGCCCGGGGATCCCCAGCTG 849

566 CCAGTGATGGTCTGGTTCCCGGGAGGCGCCTTCATCGTGGGCGCTGCTTC 615
|||||
850 CCAGTGATGGTCTGGTTCCCGGGAGGCGCCTTCATCGTGGGCGCTGCTTC 899

616 TTCGTACGAGGGCTCTGACTTGGCCGCCCGCGAGAAAAGTGGTGCTGGTGT 665
|||||
900 TTCGTACGAGGGCTCTGACTTGGCCGCCCGCGAGAAAAGTGGTGCTGGTGT 949

666 TTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGACGACAGC 715
|||||
950 TTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGACGACAGC 999

716 CACGCGCGCGGGAACTGGGGGCTGCTGGACCAGATGGCGCTCTGCGCTG 765

10/24

FIG. 4C

766 GGTGCAGGAGAACATCGCAGCCTTCGGGGGAGAGCCAGGAAATGTGACCC 815
 ||||||||||||||||||||||||||||||||||||||||||||
 1050 GGTGCAGGAGAACATCGCAGCCTTCGGGGGAGAGCCAGGAAATGTGACCC 1099
 816 TGTTCGGCCAGTCGGCGGGGGCCATGAGCATCTCAGGACTGATGATGTCA 865
 ||||||||||||||||||||||||||||||||||||||||||||
 1100 TGTTCGGCCAGTCGGCGGGGGCCATGAGCATCTCAGGACTGATGATGTCA 1149
 866 CCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCAGAGTGGCACC GC 915
 ||||||||||||||||||||||||||||||||||||||||||||
 1150 CCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCAGAGTGGCACC GC 1199
 916 GTTATTAGACTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGG 965
 ||||||||||||||||||||||||||||||||||||||||||||
 1200 GTTATTAGACTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGG 1249
 966 TTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAAC 1015
 ||||||||||||||||||||||||||||||||||||||||||||
 1250 TTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAAC 1299
 1016 TGCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGAT 1065
 ||||||||||||||||||||||||||||||||||||||||||||
 1300 TGCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGAT 1349
 1066 GAGATTCTTCCAACCTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGT 1115
 ||||||||||||||||||||||||||||||||||||||||||||
 1350 GAGATTCTTCCAACCTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGT 1399
 1116 CCATGAGCCCTGTGGTGGATGGTGTGGTGATCCAGATGACCCCTTGGTG 1165
 ||||||||||||||||||||||||||||||||||||||||||||
 1400 CCATGAGCCCTGTGGTGGATGGTGTGGTGATCCAGATGACCCCTTGGTG 1449
 1166 CTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTTCTAGGTGTCAA 1215
 ||||||||||||||||||||||||||||||||||||||||||||
 1450 CTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTTCTAGGTGTCAA 1499
 1216 CAACCTGGAATTCAATTGGCTCTTGCCCTTATATCATGAAGTTCGCCGCTAA 1265
 ||||||||||||||||||||||||||||||||||||||||||||
 1500 CAACCTGGAATTCAATTGGCTCTTGCCCTTAT..... 1530
 .
 .
 1316 CGCACCCTGTTGAATATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGA 1365
 ||||||||||||||||||||||||||||||||||||||||||||
 1531AATATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGA 1568
 1366 GTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTA 1415

GGTGCAGGAGAACATCGCAGCCTTCGGGGGAGAGCCAGGAAATGTGACCC

FIG. 4D

1416 TGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCCACTGCAGACT 1465
 ||||||||||||||||||||||||||||||||||||||||||||
 1619 TGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCCACTGCAGACT 1668
 ||||||||||||||||||||||||||||||||||||||||||||
 1466 GCTCACTACCACCGAGATGCCGGCCTCCCTGTCTACCTGTATGAATTTGA 1515
 ||||||||||||||||
 1669 GCTCACTACCACCGA..... 1683
 .
 .
 1666 CAACTTTGCCCGCACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGGC 1715
 ||||||||||||||||||||||||||||||||||||||||||||
 1684GAAACCCCAATGATGGGAATCTGCCCTGCTGGC 1716
 ||||||||||||||||||||||||||||||||||||||||||||
 1716 CACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGA 1765
 ||||||||||||||||||||||||||||||||||||||||||||
 1717 CACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGA 1766
 ||||||||||||||||||||||||||||||||||||||||||||
 1766 GTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTGGATGAGTCTGTA 1815
 ||||||||||||||||||||||||||||||||||||||||||||
 1767 GTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTGGATGAGTCTGTA 1816
 ||||||||||||||||||||||||||||||||||||||||||||
 1816 CCAGTCTCAAAGACCTGAGAAAGCAGAGGCAATTCTAAGGGTGGCTATGCA 1865
 ||||||||||||||||||||||||||||||||||||||||||||
 1817 CCAGTCTCAAAGACCTGAGAAAGCAGAGGCAATTCTAAGGGTGGCTATGCA 1866
 ||||||||||||||||||||||||||||||||||||||||||||
 1866 GGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGAC 1915
 ||||||||||||||||||||||||||||||||||||||||||||
 1867 GGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGAC 1916
 ||||||||||||||||||||||||||||||||||||||||||||
 1916 TAGCCATGGACATACCTGGGGACAAGAGTTCTACCCAAGGGCGAATTCGT 1965
 ||||||||||||||||||||||||||||||||||||||||||||
 1917 TAGCCATGGACATACCTGGGGACAAGAGTTCTACCCA...CCCCA...GT 1960
 |||||
 1966 TTAAACCTGCAGGA.CTAG..... 1983
 ||| ||||||||
 1961 TTAGAACTGCAGGAGTCCCTGCTGCCTCCAGGCCAAAGCTAGAGCTTTT 2010
 .
 .

FIG. 5A

ALIGN calculates a global alignment of two sequences
version 2.0>Please cite: Myers and Miller, CABIOS (1989)

COE-2 584 aa vs.
PRO873 545 aa

scoring matrix: BLOSUM50, gap penalties: -12/-2
62.4% identity; Global alignment score: 2271

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COE-2 M-----PST-----VLPTVLPSSLPTAG
      :          :. :. :.
pro873 MSTGFSFGSGLGTTVAAGTSTGGVFGTGTSSNPSSVGLNFGNLGSTSTPATTSAPS
      10  20  30  40  50  60

      20  30  40  50  60  70
COE-2 AGWSMRWILCWSLTLCMAQTALGALHTRKRPQVVTKYGTLOGKQMEHVGTPIQVFLGVPF
      :. :. :. :. :. :.
pro873 SGFGTGLFGSKPATGFTLGTTNTGALHTRKRPQVVTKYGTLOGKQMEHVGTPIQVFLGVPF
      70  80  90  100  110  120

      80  90  100  110
COE-2 SRPPLGILRFAPPEPEPWKGINDATYPPG-----
      :. :. :. :. :. :.
pro873 SRPPLGILRFAPPEPEPWKGINDATYPPGWSLSPGWSAVARSRLTATSASRVQASL
      130  140  150  160  170  180

      120  130  140  150
COE-2 -----CLQESWGQLASMYVSTRERYKWLRFSEDCLYLNIVYAPARAPGDPOLPVM
      :. :. :. :. :. :.
pro873 LPQPLSVGWYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNIVYAPARAPGDPOLPVM
      190  200  210  220  230  240

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FIG. 5B

160	170	180	190	200	210
COE-2	VNFPQGAIVGAASYESGDLAAREKVVLVFLQHRIGIFGFLSTDDSHARGNWGLLDQMA				
	250	260	270	280	290
pro873	VNFPQGAIVGAASYESGDLAAREKVVLVFLQHRIGIFGFLSTDDSHARGNWGLLDQMA				300
	310	320	330	340	350
220	230	240	250	260	270
COE-2	ALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMSPGLASGLFHRAISQGTALFLFI				
	310	320	330	340	350
pro873	ALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMSPGLASGLFHRAISQGTALFLFI				360
	280	290	300	310	320
COE-2	TSNPLKVAKVLAHLACGNHNSQILVNCRLALSGTKVMRYSNKMRFQLQNFQRPDEEIIW				330
	370	380	390	400	410
pro873	TSNPLKVAKVLAHLACGNHNSQILVNCRLALSGTKVMRYSNKMRFQLQNFQRPDEEIIW				420
	340	350	360	370	380
COE-2	SMSPVVDGVVTPDDPLVLTQGGKVSSVPYLLGVNNLEFNLLPYIMKFFPLNRQAMRKETI				390
	430	440	450	460	
pro873	SMSPVVDGVVTPDDPLVLTQGGKVSSVPYLLGVNNLEFNLLPY-----				
	400	410	420	430	440
COE-2	TKMLWSTRLNITKEQVPLVVEEYLDNVNEHDWKMLNRNMDIVQDATFYVYATLQTAHY				450
	470	480	490	500	510
pro873	-----NITKEQVPLVVEEYLDNVNEHDWKMLNRNMDIVQDATFYVYATLQTAHY				

COOFTIO-2220001

FIG. 5C

460	470	480	490	500	510
COE-2	HRDAGLPVLYE	FEHHARGI	IIVKPR	TDGADH	GDENYFL
:	:	:	:	:	:
:	:	:	:	:	:
:	:	:	:	:	:
pro873	HRET--PMM	-----CIC--P	-----AGHA	-----	-----
	520				
520	530	540	550	560	570
COE-2	KYWANFARTGN	PNDGNLPC	WPRYNK	DEKYLQ	LDFTTRVGM
:	:	:	:	:	:
:	:	:	:	:	:
:	:	:	:	:	:
pro873	-----	-----	-----	-----	-----
	530				
580					
COE-2	KQRQF				
:	:				
pro873	-QEW				

FIG. 6A

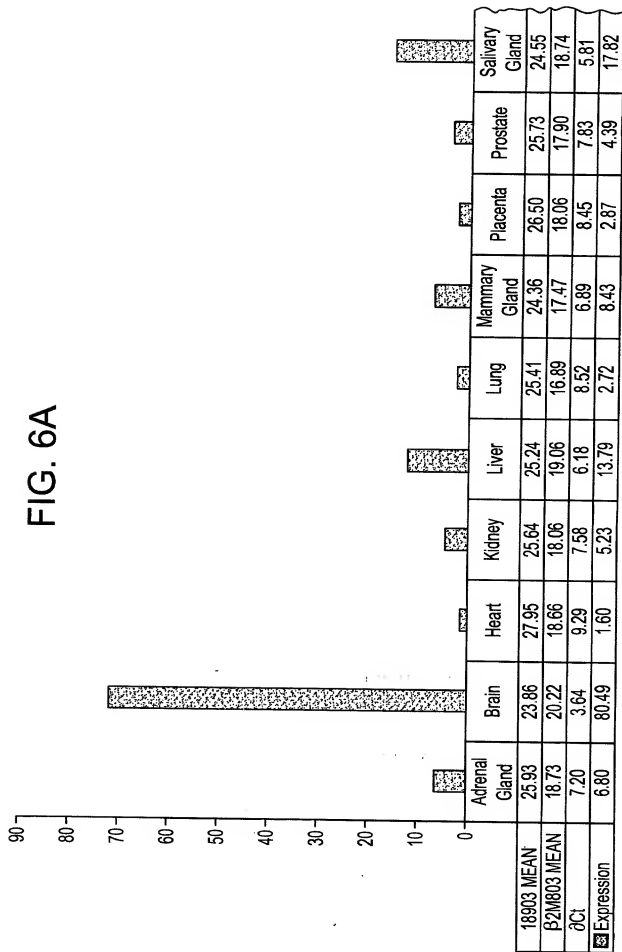


FIG. 6B

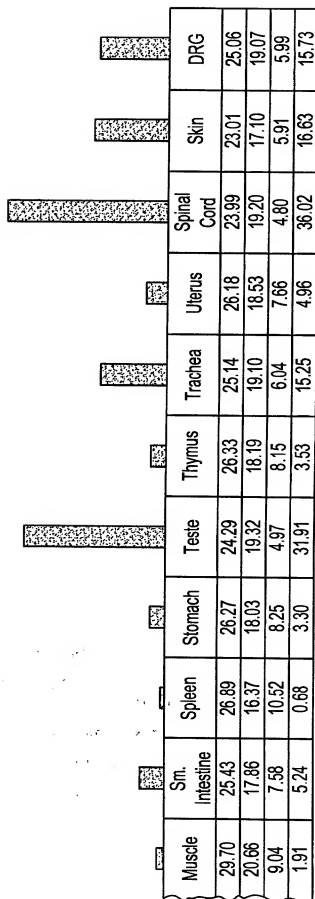


FIG. 7A

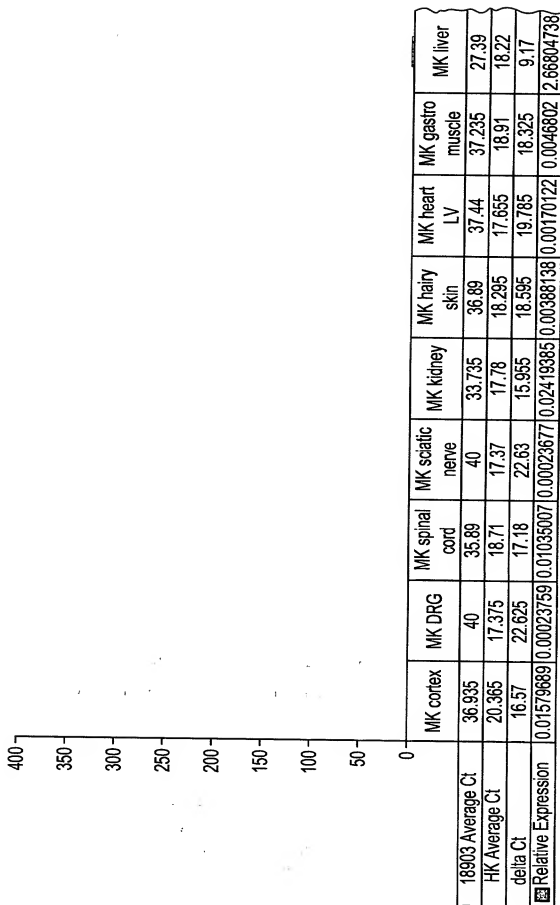


FIG. 7B

Hu. Brain	Hu. Spinal cord	Hu. Heart	Hu. Kidney	Hu. Liver	Hu. Lung
21.27	23.78	28.26	26.155	25.43	25.805
19.245	18.295	17.855	17.925	18.22	15.87
2.025	5.485	10.405	8.23	7.21	9.935
377.618146	34.3154004	1.13349992	5.11872423	10.3803579	1.57002147

FIG. 8A-1

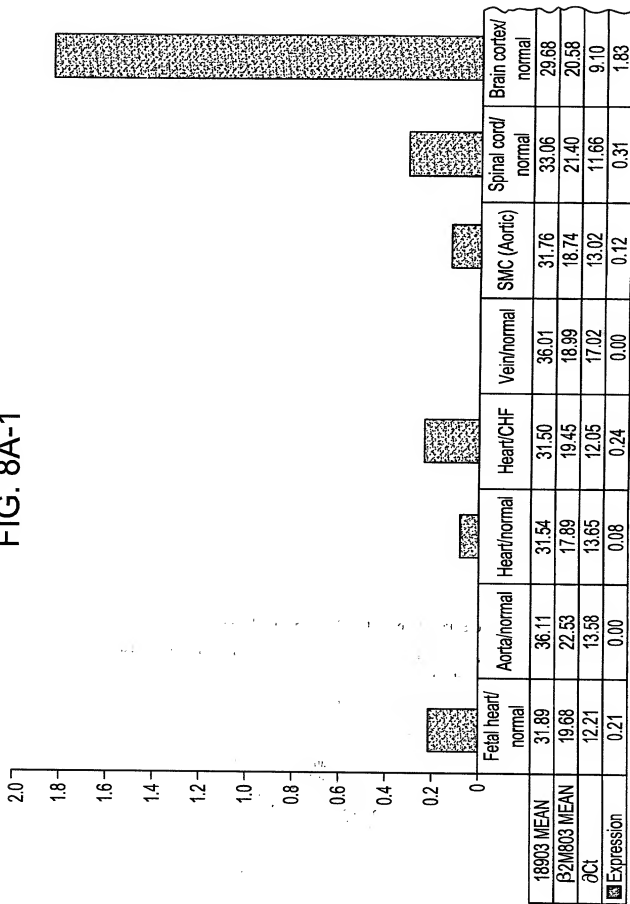


FIG. 8A-2

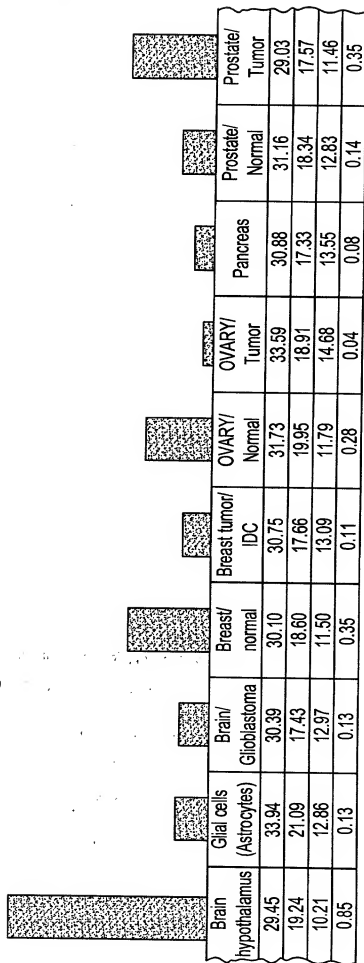


FIG. 8A-3

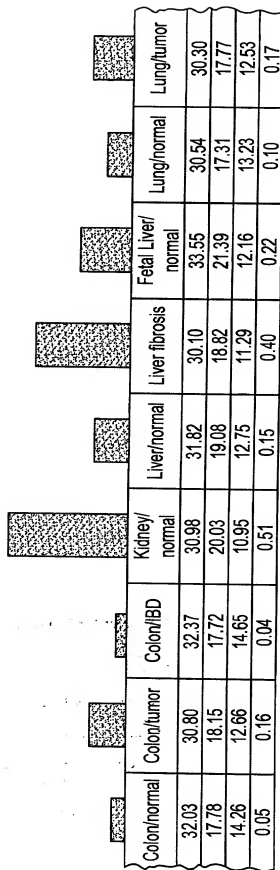
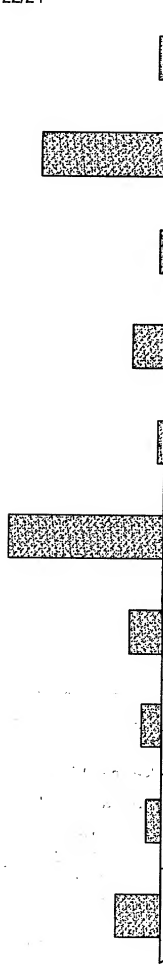


FIG. 8A-4



Lung/COPD	Tonsil/normal	Lymph node/normal	Thymus/normal	Epithelial Cells (Prostate)	Endothelial Cells (Aortic)	Skeletal Muscle	Fibroblasts (Dermal)	Skin/Normal	Adipose/Normal
29.44	31.13	31.40	32.80	30.70	35.27	31.06	33.10	31.16	32.43
17.10	17.19	17.91	20.03	20.13	20.16	18.26	18.18	20.29	17.96
12.34	13.94	13.49	12.78	10.57	15.11	12.81	14.92	10.87	14.47
0.19	0.06	0.09	0.14	0.66	0.03	0.14	0.03	0.54	0.04

FIG. 8A-5

Osteoblasts (Primary)	Osteoblasts (Undiff)	Osteoblasts (Diff)	Osteoclasts	Aorta SMC (Early)	Aorta SMC (Late)	HUVEC	HMVEC
34.84	33.19	33.23	32.47	32.50	32.72	32.17	32.74
20.44	18.50	17.83	17.25	19.53	18.77	19.27	18.74
14.40	14.69	15.40	15.22	12.97	13.96	12.91	14.00
0.05	0.04	0.02	0.03	0.13	0.06	0.13	0.06

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FIG. 8B

Tissue	18903 MEAN	β 2M803 MEAN	δ Ct	Expression
Fetal heart/normal	31.89	19.68	12.21	0.21
Aorta/normal	36.11	22.53	13.58	0.00
Heart normal	31.54	17.89	13.65	0.08
Heart/CHF	31.50	19.45	12.05	0.24
Vein/normal	36.01	18.99	17.02	0.00
SMC (Aortic)	31.76	18.74	13.02	0.12
Spinal cord/normal	33.06	21.40	11.66	0.31
Brain cortex/normal	29.68	20.58	9.10	1.83
Brain hypothalamus/normal	29.45	19.24	10.21	0.85
Glial cells (Astrocytes)	33.94	21.09	12.86	0.13
Brain/Glioblastoma	30.39	17.43	12.97	0.13
Breast/normal	30.10	18.60	11.50	0.35
Breast tumor/IDC	30.75	17.66	13.09	0.11
Ovary/normal	31.73	19.95	11.79	0.28
Ovary/tumor	33.59	18.91	14.68	0.04
Pancreas	30.88	17.33	13.55	0.08
Prostate/normal	31.16	18.34	12.83	0.14
Prostate/tumor	29.03	17.57	11.46	0.35
Colon/normal	32.03	17.78	14.26	0.05
Colon/tumor	30.80	18.15	12.66	0.16
Colon/IBD	32.37	17.72	14.65	0.04
Kidney/normal	30.98	20.03	10.95	0.51
Liver/normal	31.82	19.08	12.75	0.15
Liver/fibrosis	30.10	18.82	11.29	0.40
Fetal Liver/normal	33.55	21.39	12.16	0.22
Lung/normal	30.54	17.31	13.23	0.10
Lung/tumor	30.30	17.77	12.53	0.17
Lung/COPD	29.44	17.10	12.34	0.19
Tonsil/normal	31.13	17.19	13.94	0.06
Lymph node/normal	31.40	17.91	13.49	0.09
Thymus/normal	32.80	20.03	12.78	0.14
Epithelial Cells(prostate)	30.70	20.13	10.57	0.66
Endothelial Cells(aortic)	35.27	20.16	15.11	0.03
Skeletal Muscle/normal	31.06	18.26	12.81	0.14
Fibroblasts (Dermal)	33.10	18.18	14.92	0.03
Skin/normal	31.16	20.29	10.87	0.54
Adipose/normal	32.43	17.96	14.47	0.04
Osteoblasts (primary)	34.84	20.44	14.40	0.05
Osteoblasts (Undiff)	33.19	18.50	14.69	0.04
Osteoblasts (Diff)	33.23	17.83	15.40	0.02
Osteoblasts	32.47	17.25	15.22	0.03
Aorta SMC (Early)	32.50	19.53	12.97	0.13
Aorta SMC (Late)	32.72	18.77	13.96	0.06
HUVEC	32.17	19.27	12.91	0.13
HMVEC	32.74	18.74	14.00	0.06

40.00

40.00

0.00